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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:11:52 ; Search time 145 Seconds

(without alignments)
993.626 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGAWLVLSLWGV.....RAELNQSEEPAGESTGGP 404

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1582122 seqs, 356623098 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	100.0	404	15	US-10-309-290-96
2	338	83.7	339	14	US-10-091-019-3
3	337	83.4	330	15	US-10-309-290-98
4	337	83.4	390	15	US-10-309-290-100
5	332	82.2	332	9	US-09-872-185B-2
6	332	82.2	332	9	US-09-851-071-1
7	216	53.5	405	8	US-08-755-235-4
8	216	53.5	405	17	US-10-850-861-4
9	207	51.2	342	16	US-10-408-765A-641
10	112	27.7	112	9	US-09-872-185B-1
11	30	7.4	30	8	US-08-948-131-1
12	30	7.4	30	9	US-09-872-185B-3
13	30	7.4	30	9	US-09-872-185B-7

14	30	7.4	30	9	US-09-851-071-5
15	24	5.9	416	8	US-08-755-235-2
16	24	5.9	416	17	US-10-850-861-2
17	22	5.4	22	9	US-09-851-071-2
18	13	3.2	30	8	US-08-948-131-2
19	13	3.2	30	9	US-09-872-185B-4
20	11	2.7	30	8	US-08-948-131-3
21	11	2.7	30	9	US-09-872-185B-5
22	10	2.5	10	8	US-08-948-131-5
23	10	2.5	10	9	US-09-872-185B-8
24	10	2.5	10	9	US-09-851-071-6
25	10	2.5	30	8	US-08-948-131-4
26	10	2.5	30	9	US-09-872-185B-6
27	9	2.2	25	16	US-10-327-598-238
28	9	2.2	25	16	US-10-327-598-241
29	9	2.2	25	16	US-10-327-598-243
30	9	2.2	25	16	US-10-327-598-244
31	9	2.2	98	14	US-10-308-817-118
32	9	2.2	98	14	US-10-308-817-119
33	9	2.2	98	14	US-10-308-817-120
34	9	2.2	98	15	US-10-453-698-118
35	9	2.2	98	15	US-10-453-698-119
36	9	2.2	98	15	US-10-453-698-120
37	9	2.2	105	14	US-10-029-386-33917
38	9	2.2	108	10	US-09-848-798-51
39	9	2.2	108	10	US-09-848-798-52
40	9	2.2	108	10	US-09-848-798-53
41	9	2.2	108	10	US-09-848-798-166
42	9	2.2	112	16	US-10-327-598-809
43	9	2.2	118	16	US-10-327-598-1106
44	9	2.2	119	14	US-10-291-265-720
45	9	2.2	128	16	US-10-327-598-1098

ALIGNMENTS

RESULT 1

US-10-309-290-96
; Sequence 96, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02

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; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 96
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-96
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Query Match 100.0%; Score 404; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWAGVGAQNITARIIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAAGTAVGAWVLVLSLWAGVGAQNITARIIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
QY 61 WKVLSPOGGPNDVSARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
DB 61 WKVLSPOGGPNDVSARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
QY 121 PGKPEIVDSASELTAGVPKNVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVPKNVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEVPVLEEVL 240
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEVPVLEEVL 240
QY 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLILPEIGPQQGTYS 300
DB 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLILPEIGPQQGTYS 300
QY 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSLGTALALGILGGLTAALLIGV 360
DB 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSLGTALALGILGGLTAALLIGV 360
QY 361 ILWQRQRGEERKAPENQEEERAEELNQSEEPAGESSTGCP 404
DB 361 ILWQRQRGEERKAPENQEEERAEELNQSEEPAGESSTGCP 404
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RESULT 2
US-10-091-019-3
; Sequence 3, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
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; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-019-3

Query Match 83.7%; Score 338; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 9.4e-230;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWAGVGAQNITARIIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAAGTAVGAWVLVLSLWAGVGAQNITARIIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
QY 61 WKVLSPOGGPNDVSARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
DB 61 WKVLSPOGGPNDVSARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
QY 121 PGKPEIVDSASELTAGVPKNVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVPKNVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEVPVLEEVL 240
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEVPVLEEVL 240
QY 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLILPEIGPQQGTYS 300
DB 241 VVEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLILPEIGPQQGTYS 300
QY 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSL 338
DB 301 CVATHSSHGPOBSRAVSIIIPBEGPTAGSVGGSL 338
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RESULT 3
US-10-309-290-98
; Sequence 98, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glemnda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-290-98
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Best Local Similarity 100.0%; Pred. No. 8.1e-289;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      68  GGGFWDVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 127
Db      54  GGGFWDVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 113

QY      128 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQTRRHPTGLFT 187
Db      114 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQTRRHPTGLFT 173

QY      188 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVLEEVQVWVEPEG 247
Db      174 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVLEEVQVWVEPEG 233

QY      248 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 307
Db      234 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 293

QY      248 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 307
Db      234 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 293
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RESULT 4
US-10-309-290-100
; Sequence 100, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chikakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
```

```
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 390
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-290-100
```

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Query Match      83.4%; Score 337; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.1e-289;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      68  GGGFWDVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 127
Db      54  GGGFWDVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVRYVQIPGKPEIV 113

QY      128 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQTRRHPTGLFT 187
Db      114 DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQTRRHPTGLFT 173

QY      188 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVLEEVQVWVEPEG 247
Db      174 LOSELMVTARGGDPRTFTSCSPGLPRHRLARTAPIQPRVMEPVLEEVQVWVEPEG 233

QY      248 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 307
Db      234 AVAPGGTVTILTCVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS 293
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Db 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGPOESRAV 316

RESULT 8

US-10-850-861-4
; Sequence 4, Application US/10850861
; Publication No. US20040228855A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/10/850,861
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/08/755,235
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-10-850-861-4

Query Match 53.5%; Score 216; DB 17; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.7e-182; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVKNVKGTCVSEGSYPAGTLSWHL 160
Db 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVKNVKGTCVSEGSYPAGTLSWHL 160
QY 161 GKPLVNEKGVSKQTRRHPETGLFTLQSELMTVPARGDPRPTSCSPGLPRHRL 220
Db 161 GKPLVNEKGVSKQTRRHPETGLFTLQSELMTVPARGDPRPTSCSPGLPRHRL 220
QY 221 RTAPIQPRVWPEVPLEEVQVAVPEGGAVAGGTGVTTLTCEVPAQSPQIHMKDGVPLPL 280
Db 221 RTAPIQPRVWPEVPLEEVQVAVPEGGAVAGGTGVTTLTCEVPAQSPQIHMKDGVPLPL 280

QY 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGPOESRAV 316

Db 281 PPSVLLPILPIGPDQGTYSVCVATHSSHGPOESRAV 316

RESULT 9

US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-641

Query Match 51.2%; Score 207; DB 16; Length 342;
Best Local Similarity 100.0%; Pred. No. 4.4e-174;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 GGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 113
QY 128 DSASELTAGVKNVKGTCVSEGSYPAGTLSWHLQKPLVNEKGVSKQTRRHPETGLFT 187
Db 114 DSASELTAGVKNVKGTCVSEGSYPAGTLSWHLQKPLVNEKGVSKQTRRHPETGLFT 173
QY 188 LQSELMTVPARGDPRPTSCSPGLPRHRLRTAPIQPRVWPEVPLEEVQVAVPEGG 247
Db 174 LQSELMTVPARGDPRPTSCSPGLPRHRLRTAPIQPRVWPEVPLEEVQVAVPEGG 233
QY 248 AVAGGTGVTTLTCEVPAQSPQIHMKD 274
Db 234 AVAGGTGVTTLTCEVPAQSPQIHMKD 260

RESULT 10

US-09-872-185B-1
; Sequence 1, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-1

Query Match 27.7%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-90; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPQBLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 82
Db 1 AQNITARIGEPLVLKCKGAPKPPQBLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 60

QY 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 134

Db 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 112

RESULT 11

US-08-948-131-1
; Sequence 1, Application US/08948131
; Publication No. US20010053357A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/948,131
;; FILING DATE: 09-OCT-1997
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 53447
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0526
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-948-131-1

Query Match 7.4%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 12
US-09-872-185B-3
; Sequence 3, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-3

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 13
US-09-872-185B-7
; Sequence 7, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie

;; APPLICANT: Lamster, Ira
;; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
;; FILE REFERENCE: 0575/64080
;; CURRENT APPLICATION NUMBER: US/09/872,185B
;; CURRENT FILING DATE: 2001-06-01
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 30
;; TYPE: PRT
;; ORGANISM: Human
US-09-872-185B-7

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 14
US-09-851-071-5
; Sequence 5, Application US/09851071
; Patent No. US20020177550A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Anne Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
; FILE REFERENCE: 0575/55424-Z/JPM/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/851,071
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human
US-09-851-071-5

Query Match 7.4%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
|||
Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 15
US-08-755-235-2
; Sequence 2, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
US-08-755-235-2

Query Match 5.9%; Score 24; DB 8; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.19e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
|||
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

Search completed: December 6, 2004, 15:21:52
Job time : 147 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	340	84.2	340	2	US-08-633-148-2	Sequence 2, Appli
2	332	82.2	332	4	US-09-062-365-1	Sequence 1, Appli
3	318	78.7	318	2	US-08-633-148-4	Sequence 4, Appli
4	304	75.2	404	4	US-09-638-649-3	Sequence 3, Appli
5	216	53.5	405	4	US-08-755-235-4	Sequence 4, Appli
6	207	51.2	278	2	US-08-432-016-5	Sequence 5, Appli
7	207	51.2	278	2	US-08-684-594-5	Sequence 5, Appli
8	30	7.4	30	4	US-09-062-365-5	Sequence 5, Appli
9	30	7.4	30	4	US-08-948-131-1	Sequence 1, Appli
10	26	6.4	403	4	US-09-638-649-5	Sequence 5, Appli
11	24	5.9	416	4	US-09-638-649-1	Sequence 1, Appli
12	24	5.9	416	4	US-08-755-235-2	Sequence 2, Appli
13	22	5.4	22	4	US-09-062-365-2	Sequence 2, Appli
14	16	4.0	16	2	US-08-633-148-18	Sequence 18, Appli
15	15	3.7	15	2	US-08-633-148-12	Sequence 12, Appli
16	13	3.3	30	4	US-08-948-131-2	Sequence 2, Appli
17	11	2.7	11	2	US-08-633-148-9	Sequence 9, Appli
18	11	2.7	11	2	US-08-633-148-15	Sequence 15, Appli
19	11	2.7	30	4	US-08-948-131-3	Sequence 3, Appli
20	10	2.5	10	2	US-08-633-148-5	Sequence 5, Appli
21	10	2.5	10	2	US-08-633-148-7	Sequence 7, Appli
22	10	2.5	10	2	US-08-633-148-8	Sequence 8, Appli
23	10	2.5	10	2	US-08-633-148-11	Sequence 11, Appli
24	10	2.5	10	2	US-08-633-148-13	Sequence 13, Appli
25	10	2.5	10	2	US-08-633-148-16	Sequence 16, Appli
26	10	2.5	10	2	US-08-633-148-17	Sequence 17, Appli
27	10	2.5	10	4	US-09-062-365-6	Sequence 6, Appli

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
QY 121 PKPEIVDSASBLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180
DB 121 PKPEIVDSASBLTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180
QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQL 240
DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLTAPIQPRVWEPVPLEEVQL 240
QY 241 VVEPEGGAAGCTVTLTCEVPAQSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS 300
DB 241 VVEPEGGAAGCTVTLTCEVPAQSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS 300
QY 301 CVATHSSHGPOESRAVSIIIEPGEPTAGSVGGSLGT 340
DB 301 CVATHSSHGPOESRAVSIIIEPGEPTAGSVGGSLGT 340

RESULT 2
US-09-062-365-1
; Sequence 1, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-1

Query Match 82.2%; Score 332; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.2e-300;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWSVARVLPNG 82
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWSVARVLPNG 60
QY 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMTVPARGGDP 202
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMTVPARGGDP 180
QY 203 RTTFCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLTCEVP 262
DB 181 RTTFCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLTCEVP 240
QY 263 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS CVATHSSHGPOESRAVSIIIE 322
DB 241 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS CVATHSSHGPOESRAVSIIIE 300
QY 323 PGEPTAGSVGGSLGTALALGILGLGTA 354
DB 301 PGEPTAGSVGGSLGTALALGILGLGTA 332

RESULT 3
US-08-633-148-4

; Sequence 4, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-4

Query Match 78.7%; Score 318; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 5.9e-287;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWSVARVLPNG 82
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWSVARVLPNG 60
QY 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMTVPARGGDP 202
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHPEITGLTQSELMTVPARGGDP 180
QY 203 RTTFCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLTCEVP 262
DB 181 RTTFCSPGLPRHRLTAPIQPRVWEPVPLEEVQLVVEPEGGAAGCTVTLTCEVP 240
QY 263 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS CVATHSSHGPOESRAVSIIIE 322
DB 241 AQPSPQIHHMKOGVPLPLPSPVLLPEIGPQDQGYTS CVATHSSHGPOESRAVSIIIE 300
QY 323 PGEPTAGSVGGSLGT 340
DB 301 PGEPTAGSVGGSLGT 318

RESULT 4
US-09-638-649-3
; Sequence 3, Application US/09638649

; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
; US-09-638-649-3

Query Match 75.2%; Score 304; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.3e-274; Indels 0; Gaps 0;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 160
DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 160
QY 161 GKPLVNEKGVSVKEQTRRHPTGLFTLOSELMTVPARGGDPRTFSCSPGLPRHRL 220
DB 161 GKPLVNEKGVSVKEQTRRHPTGLFTLOSELMTVPARGGDPRTFSCSPGLPRHRL 220
QY 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
QY 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316
DB 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316

RESULT 5
US-08-755-235-4
; Sequence 4, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
; US-08-755-235-4

Query Match 53.5%; Score 216; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6e-192;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 160

DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 160
QY 161 GKPLVNEKGVSVKEQTRRHPTGLFTLOSELMTVPARGGDPRTFSCSPGLPRHRL 220
DB 161 GKPLVNEKGVSVKEQTRRHPTGLFTLOSELMTVPARGGDPRTFSCSPGLPRHRL 220
QY 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEPVLEEVQVWPEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL 280
QY 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316
DB 281 PPSFVLILPEIGPDQGTYSVATHSHGPOESRAV 316

RESULT 6
US-08-432-016-5
; Sequence 5, Application US/08432016
; Patent No. 5968768
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,016
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-432-016-5

Query Match 51.2%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7e-184;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 160
DB 72 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVGTCVSGSYPAAGTLSWHL 131

QY 161 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRL 220
DB 132 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRL 191
QY 221 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 192 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 251
QY 281 PPSPVLLILPEIGPODQGTYSVATHSS 307
DB 252 PPSPVLLILPEIGPODQGTYSVATHSS 278

RESULT 7

US-08-684-594-5

; Sequence 5, Application US/08684594

; Patent No. 5998172

; GENERAL INFORMATION:

; APPLICANT: HAYNES, BARTON P.

; APPLICANT: ARUFFO, ALEANDRO

; APPLICANT: PATEL, DHAVALKUMAR

; APPLICANT: BOWEN, MICHAEL A.

; APPLICANT: MARQUARDT, HANS

; TITLE OF INVENTION: CD6 LIGAND

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/684,594

; FILING DATE: 18-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/432,016

; FILING DATE: 01-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/333,350

; FILING DATE: 02-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/143,903

; FILING DATE: 02-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 1579-112

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 278 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-684-594-5

Query Match 51.2%; Score 207; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 5.7e-184;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTLSWHL 160

DB 72 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTLSWHL 131
QY 161 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRL 220
DB 132 GKPLVPNEKGVSVKEQTRRHPTETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRL 191
QY 221 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 192 RTAPIQPRVWBPVPLEEVQVVEPEGGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 251
QY 281 PPSPVLLILPEIGPODQGTYSVATHSS 307
DB 252 PPSPVLLILPEIGPODQGTYSVATHSS 278

RESULT 8

US-09-062-365-5

; Sequence 5, Application US/09062365

; Patent No. 6465422

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A

; FILE OF INVENTION: SUBJECT

; FILE REFERENCE: 55424

; CURRENT APPLICATION NUMBER: US/09/062,365

; CURRENT FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in ver. 2.1

; SEQ ID NO 5

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Human

; US-09-062-365-5

Query Match 7.4%; Score 30; DB 4; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52

DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 9

US-08-948-131-1

; Sequence 1, Application US/08948131

; Patent No. 655651

; GENERAL INFORMATION:

; APPLICANT: Stern, David

; APPLICANT: Yan, Shi Du

; APPLICANT: Schmidt, Ann Marie

; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/948,131

; FILING DATE: 09-OCT-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P

```
;
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 53447
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-278-0400
;   TELEFAX: 212-391-0526
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 30 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-948-131-1

Query Match          7.4%; Score 30; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIQEPLVLKCKGAPKPPQRLWK 52
Db 1 AQNITARIQEPLVLKCKGAPKPPQRLWK 30

RESULT 10
US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: US5 THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

Query Match          6.4%; Score 26; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 8.4e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTILSHWLDGK 162
Db 136 VPKVGTCTVSEGSYPAGTILSHWLDGK 161

RESULT 11
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: US5 THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
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;   ORGANISM: Bos Taurus
US-09-638-649-1

Query Match          5.9%; Score 24; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAAPGGTIVLTCE 260
Db 247 EVQLVVEPEGGAAPGGTIVLTCE 270

RESULT 12
US-08-755-235-2
; Sequence 2, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
US-08-755-235-2

Query Match          5.9%; Score 24; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAAPGGTIVLTCE 260
Db 247 EVQLVVEPEGGAAPGGTIVLTCE 270

RESULT 13
US-09-062-365-2
; Sequence 2, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; TITLE OF INVENTION: SUBJECT
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-2

Query Match          5.4%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVG 22
Db 1 MAAGTAVGAWLVLSLWGA VVG 22

RESULT 14
US-08-633-148-18
; Sequence 18, Application US/08633148
```

Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-18

Query Match 4.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLKC 38
Db 1 AQNITARIGEPLVLKC 16

RESULT 15
US-08-633-148-12
Sequence 12, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSE, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-12

Query Match 3.7%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLK 37
Db 1 AQNITARIGEPLVLK 15

Search completed: December 6, 2004, 15:19:20
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:08:06 ; Search time 45 Seconds
(without alignments)
863.813 Million cell updates/sec

Title: US-10-069-598-1
Perfect score: 404
Sequence: 1 MAAGTAGAVLVLSLWGV.....RAELNQSEPEAGESTTGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	100.0	404	1 I61596	advanced glycosyla
2	26	6.4	402	2 T09062	probable advanced
3	24	5.9	416	1 A42879	advanced glycosyla
4	9	2.2	97	2 S36066	Ig lambda chain -
5	9	2.2	98	2 S36063	Ig lambda chain -
6	9	2.2	98	2 S36062	Ig lambda chain -
7	9	2.2	110	2 S57465	Ig lambda chain V-
8	9	2.2	112	2 S26855	Ig lambda chain V
9	9	2.2	116	2 C27390	Ig lambda chain pr
10	9	2.2	117	1 LVH02	Ig lambda chain pr
11	9	2.2	117	2 S04526	Ig lambda chain pr
12	9	2.2	120	2 S30528	Ig lambda chain V
13	9	2.2	136	2 S42610	Ig lambda chain V
14	9	2.2	235	2 S25749	ARMVlambda protein
15	8	2.0	132	2 C69050	Ig lambda chain -
16	8	2.0	170	2 A87614	phycocyanin alpha
17	8	2.0	267	2 S38367	pilus assembly pro
18	8	2.0	315	2 T37901	tetrahydromethanop
19	8	2.0	357	1 K1BEBR	probable purine nu
20	8	2.0	359	1 K1BEBT	thymidine kinase (
21	8	2.0	394	2 D70674	probable lipid car
22	8	2.0	401	2 D83873	hypothetical prote
23	8	2.0	410	2 T13531	hypothetical prote
24	8	2.0	420	2 S71199	dnaj protein homol
25	8	2.0	420	2 T49127	dnaj protein homol
26	8	2.0	462	2 AB3222	two component sens
27	8	2.0	466	2 A95963	probable oxidoredu
28	8	2.0	549	2 JC5926	secreted klotho pr
29	8	2.0	550	2 G70597	probable proteinase

30 8 2.0 555 2 F72555 probable molybdenu
31 8 2.0 599 2 G86204 hypothetical prote
32 8 2.0 643 2 T50539 intermediate filam
33 8 2.0 745 2 T51370 hypothetical prote
34 8 2.0 993 2 S46779 26S proteasome reg
35 8 2.0 1012 2 JC5925 membrane klotho pr
36 8 2.0 1089 2 T31583 hypothetical prote
37 8 2.0 6831 2 A88852 protein unc-22 (im
38 8 2.0 6839 2 S57242 twitchin [similar
39 8 2.0 7160 2 T27935 hypothetical prote
40 7 1.7 89 2 G96958 ACT domain contain
41 7 1.7 105 2 E75360 conserved hypothet
42 7 1.7 106 2 I48862 tyrosine kinase gr
43 7 1.7 125 2 C72579 hypothetical prote
44 7 1.7 136 2 S74785 hypothetical prote
45 7 1.7 144 2 S23655 superoxide dismuta

ALIGNMENTS

RESULT 1
I61596
advanced glycosylation end-products receptor precursor - human
N/Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: I61596; B42879; S27968
R/Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;
Genomics 23, 408-419, 1994
A/Title: Three genes in the human MHC class III region near the junction with the class I
interpart of mouse mammary tumor gene int-3.
A/Reference number: A55562; MUID:95137587; PMID:7835890
A/Accession: I61596
A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A/Molecule type: DNA
A/Residues: 1-404 <RES>
A/Cross-references: UNIPROT:Q15109; GB:D28769; NID:G561657; PIDN:BAA05958.1; PID:G561659
R/Neepser, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; See
J. Biol. Chem. 267, 14998-15004, 1992
A/Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A/Reference number: A42879; MUID:92340547; PMID:1378843
A/Accession: B42879
A/Molecule type: mRNA
A/Residues: 'G', '2-99', 'R', '101-404 <NEE>
A/Cross-references: EMBL:M91211; NID:G190845; PIDN:AAA03574.1; PID:G190846
A/Experimental source: lung
A/Note: Sequence extracted from NCBI backbone (NCBIP:109438)
C/Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosyl
cellular function, thus contributing to tissue lesions in diabetes.
C/Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C/Genetics:
A/Gene: GDB:AGER
A/Cross-references: GDB:306354; OMIM:600214
A/Map position: 6p21.3-6p21.3
A/Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
C/Function:
A/Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit
C/Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C/Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-404/Product: advanced glycosylation end products predicted <EXT>
F/31-101/Domain: extracellular #status predicted <INT>
F/31-101/Domain: immunoglobulin homology <IM1>
F/317-210/Domain: immunoglobulin homology <IM2>
F/252-303/Domain: immunoglobulin homology <IM3>
F/345-362/Domain: transmembrane #status predicted <TMW>
F/363-404/Domain: intracellular #status predicted <INT>
F/25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/38-99,144-208,259-301/Disulfide bonds: #status predicted
Query Match 100.0%; Score 404; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPQBLEWKLNTGRTEA 60
Db 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPQBLEWKLNTGRTEA 60

Qy 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGTODEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGTODEGIFRCQAMNRNGKETKSNYRVVYQI 120

Qy 121 PKKPIVDASBELTAGVKNKVTCSSEYSPAGTILSWHLDGKPLVNEKGVSVKEQTRRH 180
Db 121 PKKPIVDASBELTAGVKNKVTCSSEYSPAGTILSWHLDGKPLVNEKGVSVKEQTRRH 180

Qy 181 PETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRALRTAPIQPRVWEPVPLEVQL 240
Db 181 PETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRALRTAPIQPRVWEPVPLEVQL 240

Qy 241 VVEPGGAVAGCTVTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTYS 300
Db 241 VVEPGGAVAGCTVTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTYS 300

Qy 301 CVATHSSHGPOBSRAVSIIIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360
Db 301 CVATHSSHGPOBSRAVSIIIEPGEPTAGSVGGSLGTALALGILGGLGTAALLIGV 360

Qy 361 ILWQRQRGERRKAPENQEEERAEALNQSEPEAGESSTGCP 404
Db 361 ILWQRQRGERRKAPENQEEERAEALNQSEPEAGESSTGCP 404

RESULT 2
T09062
Probable advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09062
R:Koren, L.; Maniatis, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>
A:Reference number: Z16543
A:Accession: T09062
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-References: UNIPROT:O35444; EMBL:AF030001; NID:G2564945; PID:G2564950
C:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.4%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 VPKVGTCTVSEGSYPAGTILSWHLDGK 162
Db 136 VPKVGTCTVSEGSYPAGTILSWHLDGK 161

RESULT 3
A42879
advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end-product-binding protein, 35K; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: A42879; A42878; S27949
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; S.

J. Biol. Chem. 267, 14998-15004, 1992
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation end-products
A:Reference number: A42879; MUID:92340547; PMID:1378843
A:Accession: A42879
A:Molecule type: mRNA
A:Residues: 1-416 <NEB>
A:Cross-References: UNIPROT:Q28173; GB:M91212; NID:G163650; PID:AAA03575.1; PID:G163651
A:Experimental source: lung
A:Note: sequence extracted from NCBI backbone (NCBI:109436)
A:Note: parts of this sequence, including the amino end of the mature protein, were detected
R:Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; Hec.
J. Biol. Chem. 267, 14987-14997, 1992
A:Title: Isolation and characterization of two binding proteins for advanced glycosylation
A:Reference number: A42878; MUID:92340546; PMID:1321822
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, X', 26-37, X', 39-49, 'XX', 52-54 <SCH>
A:Experimental source: endothelial cells
A:Note: Sequence extracted from NCBI backbone (NCBI:109434)
C:Comment: Advanced glycosylation end-products are heterogeneous nonenzymatically glycosylated
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on
aces in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Function:
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurin
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <MM>
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TMM>
F:373-416/Domain: intracellular #status predicted <INT>
F:25-80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/disulfide bonds: #status predicted

Query Match 5.9%; Score 24; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-14; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 EVQLVVEPGGAVAPGGVTLTCE 260
Db 247 EVQLVVEPGGAVAPGGVTLTCE 270

RESULT 4
S36066
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-May-1997
C:Accession: S36066
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WIL>
A:Cross-References: EMBL:222210
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 2.2%; Score 9; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.74; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 PGGTTLTLC 259
Db 14 PGGTTLTLC 22


```

RESULT 5
S36063
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36063
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22206; NID:g312867; PIDN:CAA80214.1; PID:g312868
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      251 PGGTVTILTC 259
DB      14 PGGTVTILTC 22

RESULT 6
S36062
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36062
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36062
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22205; NID:g312865; PIDN:CAA80213.1; PID:g312866
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      251 PGGTVTILTC 259
DB      14 PGGTVTILTC 22

RESULT 7
S57465
Ig lambda chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57465
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neuropathy
A;Reference number: S57408
A;Accession: S57465
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <PAT>
A;Cross-references: EMBL:X87896; NID:g871390; PIDN:CAA61147.1; PID:g871391
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 110;

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Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      251 PGGTVTILTC 259
DB      14 PGGTVTILTC 22

RESULT 8
S26655
Ig lambda chain V region (hybridoma CH4-14) - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S26655
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies: I
A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26655
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-112 <BHR>
A;Cross-references: EMBL:X65288
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      251 PGGTVTILTC 259
DB      14 PGGTVTILTC 22

RESULT 9
C27390
Ig lambda chain precursor V region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: C27390
R;Steen, M.L.; Hellman, L.; Pettersson, U.
Gene 55, 75-84, 1987
A;Title: The immunoglobulin lambda locus in rat consists of two C-lambda genes and a sing
A;Reference number: A27390; MUID:87305594; PMID:3114047
A;Accession: C27390
A;Molecule type: DNA
A;Residues: 1-116 <STE>
A;Cross-references: GB:M17092; NID:g204880; PIDN:AAA41423.1; PID:g204881
C;Genetics: 15/3
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

Query Match      2.2%; Score 9; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      251 PGGTVTILTC 259
DB      33 PGGTVTILTC 41

RESULT 10
LVH02
Ig lambda chain precursor V region (4A) - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01993; S36061
R;Anderson, M.L.M.; Szajnert, M.F.; Kaplan, J.C.; McColl, L.; Young, B.D.
Nucleic Acids Res. 12, 6647-6661, 1984

```

A:Title: The isolation of a human Ig V-lambda gene from a recombinant library of chromos
A:Reference number: A01993; MUID:85014122; PMID:6091030
A:Accession: A01993
A:Molecule type: DNA
A:Residues: 1-117 <AND>
A:Cross-references: UNIPROT:P04211
A>Note: the sequence was determined from the germline gene
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36061
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 21-117 <WIL>
A:Cross-references: EMBL:Z22204; NID:g312869; PIDN:CAA80212.1; PID:g312870
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-117/Product: Ig lambda chain V region (4A) #status predicted <MAT>
F:21-42/Region: framework 1
F:35-112/Domain: immunoglobulin homology <IMM>
F:43-55/Region: complementarity-determining 1
F:56-71/Region: framework 2
F:72-78/Region: complementarity-determining 2
F:79-110/Region: framework 3
F:111-117/Region: complementarity-determining 3
F:42-110/Disulfide bonds: #status predicted

Query Match 2.2%; Score 9; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
Db 34 PGGTVTLTC 42

RESULT 11
S04526
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04526
R:Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3975, 1989
A:Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A:Reference number: S04525; MUID:189282401; PMID:2499871
A:Accession: S04526
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <ALE>
A:Cross-references: EMBL:X14614; NID:g33406; PIDN:CAA32768.1; PID:g736247
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
C:Genetics:
A:introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
Db 33 PGGTVTLTC 41

RESULT 12
S30528
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30528
R:Mariette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAR>
A:Cross-references: EMBL:Z18334
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
Db 14 PGGTVTLTC 22

RESULT 13
S42610
ARMVlambda protein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S42610
R:Spatz, L.A.; Williams, M.; Breder, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A:Title: DNA sequence analysis and comparison of the variable heavy and light chain regi
A:Reference number: S42610; MUID:92138794; PMID:1370957
A:Accession: S42610
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <SPA>
A:Cross-references: EMBL:X54136; NID:g433485; PIDN:CAA38071.1; PID:g433486
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:39-116/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
Db 38 PGGTVTLTC 46

RESULT 14
S25749
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25749
R:Combrato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25749
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57814; NID:g33727; PIDN:CAA40951.1; PID:g33728
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 2.2% Score 9; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTVTLTC 259
|||||||
Db 33 PGGTVTLTC 41

RESULT 15
C69050
phycocyanin alpha phycocyanobilin lyase CpcE - Methanobacterium thermoautotrophicum (str
C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: C69050
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: C69050
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-132 <MTH>
A; Cross-references: UNIPROT:O27431; GB:AE000901; GB:AE000666; NID:G2622486; PIDN:AAB8585
A; Experimental source: strain Delta H
C; Genetics:
A; Gene: MTH1378
A; Start codon: GTG

Query Match 2.0% Score 8; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 ALALGILG 349
|||||||
Db 90 ALALGILG 97

Search completed: December 6, 2004, 15:18:36
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:03:46 ; Search time 192 Seconds
(without alignments)
1210.684 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGANVLVSLWGA.....RAELNQSEEPAGESTGGP 404

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	404	100.0	404	1	RAGE HUMAN
2	331	81.9	347	2	O86SN1
3	131	32.4	147	2	Q71B97
4	131	32.4	147	2	AAQ10686
5	82	20.3	82	2	Q9UQR5
6	30	7.4	50	2	Q71BB6
7	30	7.4	50	2	AAQ10685
8	30	7.4	50	2	AAQ10782
9	28	6.9	402	1	RAGE RAT
10	28	6.9	402	2	Q6MG86
11	28	6.9	402	2	CAE83960
12	26	6.4	402	2	O35444
13	26	6.4	402	2	AAH61182
14	26	6.4	403	1	RAGE MOUSE
15	24	5.9	416	1	RAGE_BOVIN
16	21	5.2	119	2	Q6TYZ6
17	21	5.2	119	2	AAQ81297
18	21	5.2	161	2	Q6UFY5
19	21	5.2	161	2	AAQ73283
20	21	5.2	330	2	Q6QP58
21	21	5.2	330	2	AA821266
22	19	4.7	23	2	Q6SA79
23	19	4.7	23	2	AA823819
24	17	4.2	17	2	Q71UQ2
25	17	4.2	17	2	AA15889
26	11	2.7	49	2	Q6SA77
27	11	2.7	49	2	AA823821
28	10	2.5	944	2	Q7SAN2
29	10	2.5	944	2	CAE85520
30	9	2.2	17	2	O95794
31	9	2.2	32	2	Q9TRQ1

32 9 2.2 117 1 LV0A HUMAN P04211 homo sapien
33 9 2.2 219 2 Q880R7 Q880r7 pseudomonas
34 9 2.2 246 2 Q9AND6 Q9anu6 pseudomonas
35 9 2.2 259 2 Q9Z171 Q9zi71 pseudomonas
36 9 2.2 261 2 Q51496 Q51496 pseudomonas
37 9 2.2 270 2 Q93874 Q93874 curvularia
38 8 2.0 17 2 Q95795 Q95795 homo sapien
39 8 2.0 99 2 Q9VAV1 Q9vav1 drosophila
40 8 2.0 132 2 O27431 O27431 methanobact
41 8 2.0 170 2 Q9L719 Q9l719 caulobacter
42 8 2.0 174 2 Q6XAR1 Q6xar1 synechococc
43 8 2.0 174 2 AAP93946 AAP93946 synechoco
44 8 2.0 192 2 Q7BNF3 Q7bnf3 anopheles g
45 8 2.0 197 2 Q6K6R2 Q6k6r2 oryza sativ

ALIGNMENTS

RESULT 1

RAGE HUMAN
ID RAGE HUMAN STANDARD; PRT; 404 AA.
AC Q15279; Q9H2X7; Q9Y3R3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=AGER; Synonyms=RAGE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=92340547; PubMed=1378843;
RA Neepner M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=95137587; PubMed=7835890;
RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
RA Inoko H., Ikemura T.;
RT "Three genes in the human MHC class III region near the junction with
RT the class II: gene for receptor of advanced glycosylation end
RT products, PBX2 homeobox gene and a notch homolog, human counterpart of
RT mouse mammary tumor gene int-3.";
RL Genomics 23:408-419(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=95137587; PubMed=7835890;
RA Banta A., Spies T., Hood L.;
RT "Sequence determination of 300 kilobases of the human class III MHC
RT locus.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.
RC MEDLINE=95137587; PubMed=7835890;
RA Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,
RA Yamamoto H.;
RT "Molecular heterogeneity of the receptor for advanced glycation
RT endproducts.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC MEDLINE=95137587; PubMed=7835890;
RA Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,
RA Schuler A., Huber G.;
RT "cDNA cloning of a novel secreted isoform of the human receptor for
RT advanced glycation end products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant

RT amyloid precursor protein.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBSJ databases.

RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lung;

RX MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242630899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [7]

RP SEQUENCE OF 1-12 FROM N.A.

RA Hudson B.I., Futers T.S.;

RT "Novel polymorphisms in the receptor for advanced glycation end-

RT products (RAGE) gene.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.

CC -!- FUNCTION: Mediates interactions of advanced glycosylation end

CC products (AGE). These are nonenzymatically glycosylated proteins

CC which accumulate in vascular tissue in aging and at an accelerated

CC rate in diabetes. Receptor for amyloid beta peptide.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).

CC Secreted (isoform 2).

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q15109-1; Sequence=Displayed;

CC Name=2; Synonyms=RAGESEC;

CC IsoId=Q15109-2; Sequence=VSP_002551, VSP_002552;

CC -!- TISSUE SPECIFICITY: Endothelial cells.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -----

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CC -----

DR EMBL; M91211; AAA03574.1; -;

DR EMBL; D28769; BAA05958.1; -;

DR EMBL; U89336; AAB47431.1; -;

DR EMBL; AB036432; BAA89369.1; -;

DR EMBL; AJ133822; CAB43108.1; -;

DR EMBL; BC020669; AAB20669.1; -;

DR EMBL; AF208289; AAG35728.1; -;

DR PIR; I61596; I61596.

DR Genew; HGNC:320; AGER.

DR MIM; 600214; -;

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_NHC.

DR Pfam; PF00047; Ig; 2.

DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Alternative splicing; Glycoprotein; Immunoglobulin domain;

KW Polymorphism; Repeat; Signal; Transmembrane.

FT SIGNAL 1 22 Potential.

FT CHAIN 23 404 Advanced glycosylation end product-

FT DOMAIN 23 342 specific receptor.

FT TRANSMEM 343 363 Extracellular (Potential).

FT DOMAIN 364 404 Potential.

FT DOMAIN 23 116 Cytoplasmic (Potential).

FT DOMAIN 124 221 Ig-like V-type.

FT DOMAIN 227 317 Ig-like C2-type 1.

FT DISULFID 38 99 Ig-like C2-type 2.

FT DISULFID 144 208 Potential.

FT DISULFID 259 301 Potential.

FT CARBOHYD 25 25 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).

FT DOMAIN 380 384 Poly-Glu.

FT VARSPLIC 54 67 Missing (in isoform 2).

FT VARSPLIC 275 404 /FTId=VSP_002551.

FT VARSPLIC 275 404 GVPLPLPSPSEVLILPEIGPQOGTYSVATSHSHGPOPSRA

FT VARSPLIC 275 404 VSIILIERGEGPTAGSVGGSLGTALALGLIGLGTAL

FT VARSPLIC 275 404 LIGVILWQRORRGEERKAPENQEEERAEALNQSEEPAG

FT VARSPLIC 275 404 ESSTGGP -> VSDLERGAGTRRGANCLRGIRAGNS

FT VARSPLIC 275 404 PGPDPGRPGDSRPAHGHVAKAATPRRGEERKPGGRG

FT VARSPLIC 275 404 GACRTESVGGT (in isoform 2).

FT VARSPLIC 275 404 /FTId=VSP_002552.

FT VARSPLIC 275 404 Q -> R.

FT VARSPLIC 275 404 /FTId=VAR_011338.

FT VARSPLIC 275 404 M -> G (in Ref. 1).

FT VARSPLIC 275 404 MM; 42802 MW; 0D584C436C30CE7 CRC64;

SQ SEQUENCE 404 AA; 42802 MW; 0D584C436C30CE7 CRC64;

Query Match 100.0%; Score 404; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGVAGWLVLSLWGAHVGAQNITARIGSEPLVLKCKGAPKPPQRLWKLTGRTEA 60

DB 1 MAAGTAGVAGWLVLSLWGAHVGAQNITARIGSEPLVLKCKGAPKPPQRLWKLTGRTEA 60

QY 61 WKVLSPQGGPWDSVARVLPNGSLPLPAVGIDEGIFRCQAMNRNGKETKSNYRVVQI 120

DB 61 WKVLSPQGGPWDSVARVLPNGSLPLPAVGIDEGIFRCQAMNRNGKETKSNYRVVQI 120

QY 121 PKGPIVDSASLTAGVKNVGTCSYSEGSYPAGTSLWHLDGKPLVNEKGVSKQTRRH 180

DB 121 PKGPIVDSASLTAGVKNVGTCSYSEGSYPAGTSLWHLDGKPLVNEKGVSKQTRRH 180

QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240

DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEVPVLEEVL 240

QY 241 VVEPGGAVAGTGTTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLILPEIGPQOGTYS 300

DB 241 VVEPGGAVAGTGTTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLILPEIGPQOGTYS 300

QY 301 CVATHSSHGPOPSRAVSIITPEGEGPTAGSVGGSLGTALALGLIGLGTALLLIGV 360

DB 301 CVATHSSHGPOPSRAVSIITPEGEGPTAGSVGGSLGTALALGLIGLGTALLLIGV 360

QY 361 ILWQRORRGEERKAPENQEEERAEALNQSEEPAGESSTGGP 404

DB 361 ILWQRORRGEERKAPENQEEERAEALNQSEEPAGESSTGGP 404

RESULT 2

Q86SN1 PRELIMINARY; PRT; 347 AA.

ID Q86SN1

AC Q86SN1;

DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

```
DE Soluble form of receptor for advanced glycation endproducts
DE precursor.
DE Name=RAGE;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGG2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1 22
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

Query Match 81.9%; Score 331; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 5.3e-311; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;

QY 1 MAAGTAGVAGWVLVLSLWGA VVGAQNI TARIGEPLVLCCKGAPKPPORLEWKLNTGRTGA 60
DB 1 MAAGTAGVAGWVLVLSLWGA VVGAQNI TARIGEPLVLCCKGAPKPPORLEWKLNTGRTGA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNRVRYQI 120
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNRVRYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSPAGTLSWHLGDKPLVPNEKGVSKQETRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSPAGTLSWHLGDKPLVPNEKGVSKQETRRH 180

QY 181 PETGLFTLQSELMTVPARGGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQL 240
DB 181 PETGLFTLQSELMTVPARGGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQL 240

QY 241 VPEEGAVAPGGTIVLTCEVPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS 300
DB 241 VPEEGAVAPGGTIVLTCEVPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS 300

QY 301 CVATHSHGQESRAVSISIIIEPEGEGTAG 331
DB 301 CVATHSHGQESRAVSISIIIEPEGEGTAG 331

RESULT 3
QY1BG7 PRELIMINARY; PRT; 147 AA.
AC QY1BG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor variant sRAGE2
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGG2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1 22
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

Query Match 81.9%; Score 331; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 5.3e-311; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;

QY 1 MAAGTAGVAGWVLVLSLWGA VVGAQNI TARIGEPLVLCCKGAPKPPORLEWKLNTGRTGA 60
DB 1 MAAGTAGVAGWVLVLSLWGA VVGAQNI TARIGEPLVLCCKGAPKPPORLEWKLNTGRTGA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNRVRYQI 120
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNRVRYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSPAGTLSWHLGDKPLVPNEKGVSKQETRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSPAGTLSWHLGDKPLVPNEKGVSKQETRRH 180

QY 181 PETGLFTLQSELMTVPARGGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQL 240
DB 181 PETGLFTLQSELMTVPARGGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQL 240

QY 241 VPEEGAVAPGGTIVLTCEVPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS 300
DB 241 VPEEGAVAPGGTIVLTCEVPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS 300

QY 301 CVATHSHGQESRAVSISIIIEPEGEGTAG 331
DB 301 CVATHSHGQESRAVSISIIIEPEGEGTAG 331

RESULT 3
QY1BG7 PRELIMINARY; PRT; 147 AA.
AC QY1BG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor variant sRAGE2
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGG2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;

Query Match 32.4%; Score 131; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.4e-118; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0;

QY 201 DPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQLVWPEGGAVPGGTIVLTCE 260
DB 1 DPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQLVWPEGGAVPGGTIVLTCE 60

QY 261 VPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS CVATHSHGQESRAVSISII 320
DB 61 VPAQPSQIHWKDGVPPLPPSPVLLIPGIDQGTYS CVATHSHGQESRAVSISII 120

QY 321 IEPGEGEGTAG 331
DB 121 IEPGEGEGTAG 131

RESULT 4
AAQ10686 PRELIMINARY; PRT; 147 AA.
ID AAQ10686;
AC AAQ10686;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor variant sRAGE2
DE (Fragment).
GN AGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22941919; PubMed=14580673;
RA Schluter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its
RT soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF536237; AAQ10686.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;

Query Match 32.4%; Score 131; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.4e-118; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0;

QY 201 DPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQLVWPEGGAVPGGTIVLTCE 260
DB 1 DPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEVQLVWPEGGAVPGGTIVLTCE 60
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QY 261 VPAQSPQIHWKGVPLPLPSPVLLIPEIGPDQGYSCVATHSHGQPSRAVSISI 320
Db 61 VPAQSPQIHWKGVPLPLPSPVLLIPEIGPDQGYSCVATHSHGQPSRAVSISI 120
QY 321 IEPGEGGTAG 331
Db 121 IEPGEGGTAG 131

RESULT 5
QY Q9UQ5 PRELIMINARY; PRT; 82 AA.
AC Q9UQ5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Receptor for advanced glycosylation end product (Fragment).
GN Name=RAGE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kankova K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238896; CAB43094.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER
SQ SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64;

Query Match 20.3%; Score 82; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.3e-71;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 PGEEGTAGSVGGSLGTALALGILGGLGTALLIGVILWQRRRGERRKAPENQEE 382
Db 1 PGEEGTAGSVGGSLGTALALGILGGLGTALLIGVILWQRRRGERRKAPENQEE 60
QY 383 EERAEINQSEEPAGESSTGGP 404
Db 61 EERAEINQSEEPAGESSTGGP 82

RESULT 6
QY Q71BB6 PRELIMINARY; PRT; 50 AA.
AC Q71BB6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor RAGE3 (Advanced glycosylation end product-specific receptor variant SRAGE1 (Fragment)).
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Breast cancer;
RL MEDLINE=22941919; PubMed=14580673;
RA Schueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF537303; AAQ10782.1; -.
DR EMBL; AF536236; AAQ10685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
```

```
FT NON TER
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;

Query Match 7.4%; Score 30; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVW 230
Db 1 DPRPTFSCSPGLPRHRALRTAPIQPRVW 30

RESULT 7
AAQ10685 PRELIMINARY; PRT; 50 AA.
AC AAQ10685;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor variant SRAGE1 (Fragment).
DE (Fragment).
GN AGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22941919; PubMed=14580673;
RA Schueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF536236; AAQ10685.1; -.
DR Receptor.
FT NON TER
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;

Query Match 7.4%; Score 30; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVW 230
Db 1 DPRPTFSCSPGLPRHRALRTAPIQPRVW 30

RESULT 8
AAQ10782 PRELIMINARY; PRT; 50 AA.
AC AAQ10782;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor RAGE3 (Fragment).
DE (Fragment).
GN AGER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Breast cancer;
RL MEDLINE=22941919; PubMed=14580673;
RA Schueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF537303; AAQ10782.1; -.
DR Receptor.
FT NON TER
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;
```


OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
 RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.,
 RA "The genomic sequence and comparative analysis of the rat major
 RT histocompatibility complex.";
 RL Genome Res. 14:631-639(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
 RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
 RA Sudbrak R., Reinhardt R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX883044; CAE83960.1; -;
 KW Receptor.
 SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;
 Query Match 6.9%; Score 28; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 6.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VPKVGTCTVSGSYGAGTSLWHLGKPL 164
 DB 136 VPKVGTCTVSGSYGAGTSLWHLGKPL 163
 RESULT 12
 O35444
 ID O35444 PRELIMINARY; PRT; 402 AA.
 AC O35444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RAGE (Advanced glycosylation end product-specific receptor).
 GN Name=RAGE; Synonyms=Ager;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14656967;
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
 RA Campbell R.D., Hood L.;
 RA "Analysis of the gene-dense major histocompatibility complex class III
 RT region and its comparison to mouse.";
 RL Genome Res. 13:2621-2636(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030001; AAB92007.1; -;
 DR EMBL: BC061182; AAB61182.1; -;
 DR PIR: T09062; T09062.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; ig; 2.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS00835; IG LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;
 Query Match 6.4%; Score 26; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 5.5e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VPKVGTCTVSGSYGAGTSLWHLGK 162
 DB 136 VPKVGTCTVSGSYGAGTSLWHLGK 161
 RESULT 13
 AAB61182
 ID AAB61182 PRELIMINARY; PRT; 402 AA.
 AC AAB61182;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Advanced glycosylation end product-specific receptor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC061182; AAH61182.1; -.
KW Receptor.
SQ SEQUENCE 402 AA; 42653 MW; DBFDC50AC8CB902 CRC64;

Query Match
Best Local Similarity 6.4%; Score 26; DB 2; Length 402;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTLSWHLGDK 162
DB 136 VPKVGTCTVSEGSYPAGTLSWHLGDK 161

RESULT 14
RAGE_MOUSE STANDARD; PRT; 403 AA.
AC Q62151;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name: Ager; Synonyms: RAGE;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=97368045; PubMed=9224812;
RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,
RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
RT "Recombinant advanced glycation end product receptor pharmacokinetics
RT in normal and diabetic rats.";
RL Mol. Pharmacol. 52:54-62(1997).
CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
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FT DOMAIN 234 316
FT DISULFID 38 98
FT DISULFID 143 207
FT DISULFID 258 300
FT CARBOHYD 25 25
FT CARBOHYD 80 80
SQ SEQUENCE 403 AA; 42668 MW; 1279796FDD1579357 CRC64;

Query Match
Best Local Similarity 6.4%; Score 26; DB 1; Length 403;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTLSWHLGDK 162
DB 136 VPKVGTCTVSEGSYPAGTLSWHLGDK 161

RESULT 15
RAGE_BOVIN STANDARD; PRT; 416 AA.
AC Q28173;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name: Ager; Synonyms: RAGE;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378843;
RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

FT DOMAIN 23 352 Extracellular (Potential).
FT TRANSMEM 353 373 Potential.
FT DOMAIN 374 416 Cytoplasmic (Potential).
FT DOMAIN 23 115 Ig-like V-type.
FT DOMAIN 123 220 Ig-like C2-type 1.
FT DOMAIN 238 327 Ig-like C2-type 2.
FT DISULFID 38 98 Potential.
FT DISULFID 143 207 Potential.
FT DISULFID 269 311 Potential.
FT CARBOHYD 25 25 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 80 80 N-linked (GlcNAc. . .) (Potential).
FT DOMAIN 391 396 Poly-Glu.
SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;

Query Match 5.9%; Score 24; DB 1; Length 416;
Best Local Similarity 100.0%; Fred. No. 4.9e-14; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
|||
Db 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

Search completed: December 6, 2004, 15:17:45
Job time : 195 secs

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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:02:58 ; Search time 157 Seconds

(without alignments)
923.100 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAVGAWVLVSLWGV.....RAELNQSEEPAGESSITGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	100.0	404	4 AAB81925	Aab1925 Extracorp
2	404	100.0	404	5 ABP65011	Abp65011 Human pro
3	404	100.0	404	8 ADF31292	Adf31292 Human rec
4	404	100.0	404	8 ADF42983	Adf42983 Human rec
5	404	100.0	404	8 ADK00129	Adk00129 Human RAG
6	403	99.8	404	5 AAM48745	Aam48745 Human RAG
7	402	99.5	402	7 ADE95564	Ad95564 Human NOV
8	373	92.3	391	8 ADP19666	Adp19666 Human LP2
9	340	84.2	340	2 AAW44199	Aaw44199 Human sol
10	340	84.2	340	2 AAW33753	Aaw33753 Human RAG
11	338	83.7	339	5 AAM48746	Aam48746 Human SRA
12	338	83.7	339	5 ABB82164	Abb82164 Human sol
13	337	83.4	330	7 ADE95566	Ad95566 Human NOV
14	337	83.4	330	7 ADE95568	Ad95568 Human NOV
15	337	83.4	330	8 ADP19670	Adp19670 Human LP2
16	337	83.4	421	6 ABR43188	Ab43188 Human REM
17	331	81.9	347	5 ABB82298	Abb82298 Human sol
18	331	81.9	347	7 ADG37044	Adg37044 Receptor
19	331	81.9	352	8 ADP19656	Adp19656 Human LP2
20	318	78.7	318	2 AAW44200	Aaw44200 Human mat
21	318	78.7	318	2 AAW33754	Aaw33754 Human RAG
22	304	75.2	404	5 AAU77543	Aau77543 Human rec
23	304	75.2	404	5 AAE23219	Aae23219 Human rec
24	304	75.2	404	7 AAE39510	Aae39510 Human RAG
25	304	75.2	404	7 ADG32004	Adg32004 Human hom

ALIGNMENTS

RESULT 1

AAB81925
ID AAB81925 standard; protein; 404 AA.

XX AC AAB81925;

XX AC AAB81925;

DT 15-JUN-2001 (first entry)

XX DE Extracorporeal circulation material receptor protein.

XX DE Extracorporeal circulation material receptor protein.

KW Extracorporeal circulation; carbonyl stress product; receptor; diabetes;
KW Vascular lesion; excretory dysfunction.

XX OS Unidentified.

XX PN WO200118060-A1.

XX PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-JP006172.

XX PR 08-SEP-1999; 99JP-00254463.

XX (TORA) TORAY IND INC.

XX PI Shimizu S, Kubota M, Akiyama H, Usui M;

XX WPI; 2001-290314/30.

XX Material for extracorporeal circulation, applicable in selective
PT elimination of diabetic complication factors such as carbonyl stress
PT products caused by abnormally promoted carbonyl stress from excretory
PT dysfunction in vascular lesions.

XX Claim 1; Page 31-32; 36pp; Japanese.

CC The present invention describes a material for extracorporeal circulation
CC which is made from a water-insoluble carrier immobilized with a protein
CC having the sequence shown here. The materials of the invention, including
CC adsorbents, are for extracorporeal circulation, which are applicable in
CC the selective elimination of diabetic complication factors from a body
CC fluid, and are therefore useful in treating vascular lesions like
CC arteriosclerosis due to carbonyl stress products caused by abnormally
CC promoted carbonyl stress from excretory dysfunction

XX SQ Sequence 404 AA;

Query Match 100.0%; Score 404; DB 4; Length 404;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNI TARI GEPLV LKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNI TARI GEPLV LKCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPVG IODEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPVG IODEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PKGPIVDSASBLTAGVPNKVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
DB 121 PKGPIVDSASBLTAGVPNKVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSFGLPRHRALRTAPIQPRVMEVPVLEEVOL 240
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCSFGLPRHRALRTAPIQPRVMEVPVLEEVOL 240

QY 241 VVEPGGAVAPCGTTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTVS 300
DB 241 VVEPGGAVAPCGTTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTVS 300

QY 301 CVATHSSHGHPQESRAVSISIIIEPGEPTAGSVGSGLTALALGILGLGTAALLIGV 360
DB 301 CVATHSSHGHPQESRAVSISIIIEPGEPTAGSVGSGLTALALGILGLGTAALLIGV 360

QY 361 ILWQRRORRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
DB 361 ILWQRRORRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404

RESULT 2
ID ABP65011 standard; protein; 404 AA.
XX AC ABP65011;
DT 25-FEB-2003 (first entry)
XX DE Human protein SEQ ID 671.
KW Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.
XX OS Homo sapiens.
XX PN WO200259260-A2.
XX PD 01-AUG-2002.
XX PP 16-NOV-2001; 2001WO-US042950.
XX PR 17-NOV-2000; 2000US-00714936.
XX PA (HYSE-) HYSEQ INC.
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-590824/63.
XX DR N-PSDB; ABQ99597.
XX PT New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX

PS Claim 20; SEQ ID NO 671; 394pp; English.

XX The present invention relates to novel human coding sequences (ABQ99268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotent state
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
CC reactions and conditions, coagulation disorders, or cancer. The
CC polynucleotide sequences of the invention were assembled from ESTs
CC isolated mainly by sequencing by hybridisation, and in some cases,
CC sequences obtained from one or more public databases. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 404 AA;

Query Match 100.0%; Score 404; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNI TARI GEPLV LKCKGAPKPPORLEWKLNTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNI TARI GEPLV LKCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPVG IODEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPVG IODEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PKGPIVDSASBLTAGVPNKVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180
DB 121 PKGPIVDSASBLTAGVPNKVGTCSVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSFGLPRHRALRTAPIQPRVMEVPVLEEVOL 240
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCSFGLPRHRALRTAPIQPRVMEVPVLEEVOL 240

QY 241 VVEPGGAVAPCGTTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTVS 300
DB 241 VVEPGGAVAPCGTTLTCEVPAQSPQIHWMDGVPLPLPSPVLLIPEIGPQOGTVS 300

QY 301 CVATHSSHGHPQESRAVSISIIIEPGEPTAGSVGSGLTALALGILGLGTAALLIGV 360
DB 301 CVATHSSHGHPQESRAVSISIIIEPGEPTAGSVGSGLTALALGILGLGTAALLIGV 360

QY 361 ILWQRRORRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404
DB 361 ILWQRRORRGERKAPENQEEERAEALNQSEEPAGESSTGGP 404

RESULT 3
ID ADF31292 standard; protein; 404 AA.
XX AC ADF31292;
XX DT 12-FEB-2004 (first entry)
XX DE Human receptor of advanced glycation end products (RAGE).

XX human; receptor; advanced glycation end product; RAGE;
 KW receptor of advanced glycation end product; high yield; high purity.
 XX Homo sapiens.
 OS JP2003306500-A.
 PN 28-OCT-2003.
 PD 05-FEB-2003; 2003JP-00027992.
 PF 15-FEB-2002; 2002JP-00038380.
 PR (TORA) TORAY IND INC.
 PA WPI; 2004-015267/02.
 DR Purifying receptor of advanced glycation end products derivative
 XX containing Igv domain of receptor of advanced glycation end product using
 PT one or more affinity columns.
 PT

XX Disclosure; SEQ ID NO 1; 13pp; Japanese.
 XX The invention relates to a method of purifying a receptor of advanced
 CC glycation end products (RAGE) derivative. The method is useful for
 CC purifying receptor of advanced glycation end product derivative. The
 CC method enables simple, rapid with high yield and high purity manufacture
 CC of RAGE derivative. The present sequence represents the amino acid
 CC sequence of human receptor of advanced glycation end products (RAGE).
 XX

Seq Sequence 404 AA;
 Query Match 100.0%; Score 404; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAVMWLVLSLWGAVVGAQNIITARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 DB 1 MAAGTAGAVMWLVLSLWGAVVGAQNIITARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 QY 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEEVL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEEVL 240
 QY 241 VPEPEGGAVAPGGTIVTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 DB 241 VPEPEGGAVAPGGTIVTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 QY 301 CVATHSHGQESRAVSIISIEPGEETAGSVGGSLGTALALGILGGLGTAALLIGV 360
 DB 301 CVATHSHGQESRAVSIISIEPGEETAGSVGGSLGTALALGILGGLGTAALLIGV 360
 QY 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404
 DB 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404

RESULT 4

ADF42983 standard; protein; 404 AA.

XX ADF42983;

XX 12-FEB-2004 (first entry)

XX Human receptor of advanced glycation (RAGE) protein.
 DE diabetec complication factor; receptor of advanced glycation end product;
 XX RAGE binding substance adsorption ligand; water-insoluble carrier;
 KW biological evaluation; diabetic complication; renal-disease; human.
 XX Homo sapiens.
 OS JP2003306499-A.
 PN 28-OCT-2003.
 PD 05-FEB-2003; 2003JP-00027991.
 PF 15-FEB-2002; 2002JP-00038378.
 PR (TORA) TORAY IND INC.
 PA WPI; 2004-015266/02.
 DR Obtaining diabetic complication factor comprises contacting biological
 XX fluid with adsorbent, and immobilizing receptor of advanced glycation end
 PT products binding substance ligand on carrier.
 PT Disclosure; SEQ ID NO 1; 18pp; Japanese.
 XX This invention relates to a novel method of obtaining a diabetic
 CC complication factor which comprises contacting liquid from a biological
 CC fluid with an adsorbent which immobilises a receptor of advanced
 CC glycation end products (RAGE) binding substance adsorption ligand on a
 CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,
 CC separating and recovering the diabetic complication factor by contacting
 CC the adsorbent with the aqueous solution. The method is useful for
 CC carrying out biological evaluation which involves determining advanced
 CC degree of diabetic complication or degree of a renal-disease.
 XX

Seq Sequence 404 AA;

Query Match 100.0%; Score 404; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAVMWLVLSLWGAVVGAQNIITARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 DB 1 MAAGTAGAVMWLVLSLWGAVVGAQNIITARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 QY 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEEVL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEPVPLEEVL 240
 QY 241 VPEPEGGAVAPGGTIVTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 DB 241 VPEPEGGAVAPGGTIVTLTCEVPAQSPQIHMWDGVPPLPPSPVLLPIGPDQGTYS 300
 QY 301 CVATHSHGQESRAVSIISIEPGEETAGSVGGSLGTALALGILGGLGTAALLIGV 360
 DB 301 CVATHSHGQESRAVSIISIEPGEETAGSVGGSLGTALALGILGGLGTAALLIGV 360
 QY 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404
 DB 361 ILWQRORRGEERKAPENQEEERAEINQSEEPAGESSTGGP 404

RESULT 5

QY 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGTALALGILGLTAALLIGV 360
 Db |||||
 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGTALALGILGLTAALLIGV 360
 QY 361 ILWQRQRGRKAPENQEEERAEALNQSEPRAGESSTG 402
 Db |||||
 361 ILWQRQRGRKAPENQEEERAEALNQSEPRAGESSTG 402

RESULT 8

ADP19666

ID ADP19666 standard; protein; 391 AA.

XX AC

ADP19666;

DT 12-AUG-2004 (first entry)

XX DE

Human LP2005 protein SEQ ID NO:12.

XX KW

human; LP2005; antidiabetic; neuroprotective; nontropic;

KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;

KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;

KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;

KW systemic lupus erythematosus.

XX OS

Homo sapiens.

XX PH

Key Location/Qualifiers

FT Peptide

1..23 /label= signal

FT Protein

24..391 /label= LP2005

XX FT

WO2004044126-A2.

XX FN

27-MAY-2004.

XX PD

05-NOV-2003; 2003WO-US032734.

XX PF

14-NOV-2002; 2002US-0426253P.

XX PR

(ELIL) LILLY & CO ELI.

XX PA

Na S, Perkins DR;

XX PI

WPI; 2004-411705/38.

XX DR

N-PSDB; ADP19665.

XX XX

PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.

XX PS

Claim 9; SEQ ID NO 12; ilpp; English.

XX CC

The present sequence represents human LP2005, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (I) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (I); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid

CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nontropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

Sequence 391 AA;

SQ

Query Match 92.3%; Score 373; DB 8; Length 391;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGPLVKCKGAPKPPORLEWLKNTGRTEA 60

Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGPLVKCKGAPKPPORLEWLKNTGRTEA 60

QY 61 WKVLSFGGGPMDVSARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

Db 61 WKVLSFGGGPMDVSARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PKPEIVDSASELTAGVKNKVTCSSESPAGTISWHLDGKPLVPNEKGVSKQETRRH 180

Db 121 PKPEIVDSASELTAGVKNKVTCSSESPAGTISWHLDGKPLVPNEKGVSKQETRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSFSGPLPRHRLTAPIQPRVWEVPLEEVQL 240

Db 181 PETGLFTLQSELMTVPARGDPRPTFSCSFSGPLPRHRLTAPIQPRVWEVPLEEVQL 240

QY 241 VVEPEGGAAPGVTTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLIPEIGPQDQGTYS 300

Db 241 VVEPEGGAAPGVTTLTCEVPAQSPQIHWKMDGVPLPLPSPVLLIPEIGPQDQGTYS 300

QY 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGTALALGILGLTAALLIGV 360

Db 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGTALALGILGLTAALLIGV 360

QY 361 ILWQRQRGRGER 373

Db 361 ILWQRQRGRGER 373

RESULT 9

AAW44199

ID AAW44199 standard; protein; 340 AA.

XX AC

AAW44199;

XX XX

14-MAY-1998 (first entry)

XX DT

Human soluble receptor to an advanced glycosylation end product.

XX DE

Human; soluble receptor; advanced glycosylation end product; AGE; antibody; vascular permeability; diabetes mellitus.

XX KW

Homo sapiens.

XX OS

WO9739125-A1.

XX FN

PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-EP001834.
 XX
 PR 16-APR-1996; 96US-00633148.
 XX
 PA (SCHD) SCHERING PATENTE AG.
 XX
 PI Morser MJ, Nagashima M, Hollander DA;
 XX
 DR WPI; 1997-558580/51.
 DR N-PSDB; AAV12394.
 XX
 PT Anti-advanced glycosylation end product polypeptide antibody - prevents
 PT receptor binding and therefore reduces vascular permeability, useful to
 PT treat diabetes mellitus.
 XX
 PS Claim 2; Page 40-41; 90pp; English.
 XX
 CC The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue
 CC in ageing, and at an accelerated rate in individuals with diabetes. The
 CC Ab, which prevents the interaction between an AGE and it's receptor
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation
 CC and purification of human RAGE polypeptide
 XX
 SQ Sequence 340 AA;
 Query Match 84.2%; Score 340; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-300;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 Db 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 QY 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 Db 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 Db 181 PETGLFTLQSELMTVPARGGDRPTTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 QY 241 VPEPEGAVAPGGTTLTCEVPAQPSQIHMKGDVLPPLPPSVLILPEIGPDQGTYS 300
 Db 241 VPEPEGAVAPGGTTLTCEVPAQPSQIHMKGDVLPPLPPSVLILPEIGPDQGTYS 300
 QY 301 CVATHSSHGQESRAVSIIEPGEEGPTAGSVGGSLGT 340
 Db 301 CVATHSSHGQESRAVSIIEPGEEGPTAGSVGGSLGT 340
 RESULT 10
 AAW33753
 ID AAW33753 standard; protein; 340 AA.
 XX
 AC AAW33753;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Human RAGE polypeptide (340 amino acid residues).
 XX

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9739121-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-EP001832.
 XX
 PR 16-APR-1996; 96US-00633147.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Morser MJ, Nagashima M;
 XX
 DR WPI; 1997-526458/48.
 DR N-PSDB; AAV06517.
 XX
 PT New soluble advanced glycosylation end-product receptor polypeptide -
 PT used for reducing vascular permeability, complications of diabetes etc.,
 PT also for purification and to screen for modulators.
 XX
 PS Claim 3; Fig 1A; 91pp; English.
 XX
 CC This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes
 XX
 SQ Sequence 340 AA;
 Query Match 84.2%; Score 340; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-300;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 Db 1 MAAGTAGAWVLVLSLWGVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTGA 60
 QY 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGGFWDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 Db 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPAAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 Db 181 PETGLFTLQSELMTVPARGGDRPTTSCSPGLPRHRLARTAPIQPRVWEPVPLEVQL 240
 QY 241 VPEPEGAVAPGGTTLTCEVPAQPSQIHMKGDVLPPLPPSVLILPEIGPDQGTYS 300
 Db 241 VPEPEGAVAPGGTTLTCEVPAQPSQIHMKGDVLPPLPPSVLILPEIGPDQGTYS 300

```

QY 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGT 340
DB 301 CVATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLGT 340

RESULT 11
ID AAM48746
XX AAM48746 standard, protein; 339 AA.
AC AAM48746;
XX
XX 02-APR-2002 (first entry)
DT
DE Human sRAGE protein SEQ ID NO 2.
XX
XX Human; RAGE; receptor for advanced glycosylated endproduct; receptor;
KW antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic;
KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;
KW Alzheimer's disease; cancer; inflammation; kidney failure;
XX systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WC200192892-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017447.
XX
XX 30-MAY-2000; 2000US-0207342P.
XX
XX 05-MAR-2001; 2001US-00799152.
XX
XX (TRAN-) TRANS TECH PHARMA.
XX
XX Shahbaz M;
PI
PI WPI; 2002-114372/15.
DR
DR
DR Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
PT for treating e.g., cancer, diabetes or inflammation, comprises measuring
PT the amount of bound anti-RAGE antibody.
XX
XX Claim 2; Fig 2; 49pp; English.
XX
XX The invention relates to detecting receptor for advanced glycosylated
CC endproducts (RAGE) modulators comprising determining the amount of RAGE
CC protein or its fragment bound to the pre-adsorbed ligand by measuring the
CC amount of anti-RAGE antibody bound to the solid surface. The method is
CC useful for rapid, high-throughput identification of compounds that
CC modulate RAGE. The compounds are useful for treating symptoms of diabetes
CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's
CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis
CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
XX
XX Sequence 339 AA;

Query Match 83.7%; Score 338; DB 5; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.5e-298;
Matches 338; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTAGANVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTAW 61
DB 2 AAGTAGANVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTAW 61

QY 62 KVLSPQGGPFWDSVARVLNGLSFLPAVGIQDEGIPRCQAMNRNGHETKSNTRVRVYQIP 121
DB 62 KVLSPQGGPFWDSVARVLNGLSFLPAVGIQDEGIPRCQAMNRNGHETKSNTRVRVYQIP 121

QY 122 GXPEIVDSASELTAGVPNKVGTCTVSGSPAGTLSMHLDGKPLVPNEKGVSKVQTRRHP 181
DB 122 GXPEIVDSASELTAGVPNKVGTCTVSGSPAGTLSMHLDGKPLVPNEKGVSKVQTRRHP 181

182 ETGLFTLQSELMTVPARGDPRPTSCSPGLPRHRLRTAPIOPRVWEPVLEEVQLV 241
DB 182 ETGLFTLQSELMTVPARGDPRPTSCSPGLPRHRLRTAPIOPRVWEPVLEEVQLV 241

242 VEPEGGAVAPGGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 301
DB 242 VEPEGGAVAPGGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 301

302 VATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLG 339
DB 302 VATHSHGQPSRAVSISIIIEPGEPTAGSVGGSLG 339

RESULT 12
ABB82164
ID ABB82164 standard; protein; 339 AA.
XX
XX ABB82164;
AC
XX 23-DEC-2002 (first entry)
DT
XX Human soluble RAGE (sRAGE).
DE
XX Receptor for Advanced Glycosylated end product; RAGE; recombinant; nootropic;
KW antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2002070667-A2.
XX
XX 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US006881.
XX
XX 05-MAR-2001; 2001US-0273418P.
XX
XX (TRAN-) TRANSTECH PHARMA INC.
XX
XX Harris R, Shen J, Shahbaz M;
PI
PI WPI; 2002-713443/77.
DR
DR N-PSDB; ABQ79956.
XX
XX High level expression of recombinant Receptors for Advanced Glycosylated end
PT Products (RAGE) proteins for treating increased levels of advanced
PT glycosylation end products, comprises infecting cells with a high titer
PT recombinant virus.
XX
XX Example; Fig 2B; 51pp; English.
XX
XX The invention relates to a method for high level expression of
CC recombinant forms of the Receptor for Advanced Glycosylated end products
CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a
CC high titer stock of recombinant virus; and (iii) infecting host cells
CC with the high titer recombinant virus under conditions such that
CC predetermined levels of RAGE or its fragment is produced, where the
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
CC per liter of culture. The method is useful for high level expression of
CC recombinant RAGE polypeptide or its fragment which may be useful in
CC preventing, treating or ameliorating diseases associated with increased
CC levels of advanced glycosylation end products, such as atherosclerosis,
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
CC nephritis, cancer or erectile dysfunction. The present sequence
CC represents the amino acid sequence of human sRAGE (soluble, extracellular
CC portion of RAGE)
XX
XX Sequence 339 AA;
SQ
Query Match 83.7%; Score 338; DB 5; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.5e-298;

```

Matches	338;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MAAGTAVGAWVLVLSLWGAVVGAQNTITARIGEPVLVKCKGAPKPKQRLWKLNTRTEA	60						
Db	1	MAAGTAVGAWVLVLSLWGAVVGAQNTITARIGEPVLVKCKGAPKPKQRLWKLNTRTEA	60						
QY	61	WKVLSPGGGFWDSVARVLVNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI	120						
Db	61	WKVLSPGGGFWDSVARVLVNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI	120						
QY	121	PGKPEIIVDSASELTAGVPNKVGTCSVSGSYGSGSPAGTLSLWHLDDGKPLVNEKGVSVKEQTRRH	180						
Db	121	PGKPEIIVDSASELTAGVPNKVGTCSVSGSYGSGSPAGTLSLWHLDDGKPLVNEKGVSVKEQTRRH	180						
QY	181	PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEVPVLEEVLQ	240						
Db	181	PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWEVPVLEEVLQ	240						
QY	241	VVEPEGGAAPGGTVTLTCEVPAQSPQIHHMKDGVPLPLPSPVLIILPEIQPDQGYTS	300						
Db	241	VVEPEGGAAPGGTVTLTCEVPAQSPQIHHMKDGVPLPLPSPVLIILPEIQPDQGYTS	300						
QY	301	CVATHSHSGPOESRAVSISIIIEPGEETAGSVGGSGL	338						
Db	301	CVATHSHSGPOESRAVSISIIIEPGEETAGSVGGSGL	338						
RESULT 13									
ADE95566									
ID	ADE95566 standard; protein; 390 AA.								
XX	ADE95566;								
XX	12-FEB-2004 (first entry)								
XX	Human NOV16d protein.								
XX	NOVX protein; biochemical stimulation; physiological stimulation;								
KW	cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;								
KW	anti-rheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;								
KW	immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;								
KW	nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;								
KW	anti-depressant; antiallergic; gynaecological; gene therapy; vaccine;								
KW	NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;								
KW	cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;								
KW	psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;								
KW	Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;								
KW	depression; allergy; fertility disorder; NOV16d.								
XX	Homo sapiens.								
OS	WO2003050245-A2.								
XX	19-JUN-2003.								
PD	03-DEC-2002; 2002WO-0308594.								
XX	05-DEC-2001; 2001US-0336600P.								
XX	07-DEC-2001; 2001US-0338285P.								
PR	12-DEC-2001; 2001US-0341346P.								
PR	17-DEC-2001; 2001US-0341477P.								
PR	17-DEC-2001; 2001US-0341540P.								
PR	20-DEC-2001; 2001US-0342592P.								
PR	27-DEC-2001; 2001US-0344297P.								
PR	31-DEC-2001; 2001US-0344903P.								
PR	17-APR-2002; 2002US-0373288P.								
PR	15-MAY-2002; 2002US-0380981P.								
PR	17-MAY-2002; 2002US-0381495P.								
PR	28-MAY-2002; 2002US-0383534P.								
PR	28-MAY-2002; 2002US-0383744P.								
PR	29-MAY-2002; 2002US-0383829P.								
PR	29-MAY-2002; 2002US-0384024P.								
PR	07-AUG-2002; 2002US-0401788P.								

Db 354 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 390

RESULT 14

ADP95568

ID ADE95568 standard; protein; 390 AA.

XX ADE95568;

AC

XX 12-FEB-2004 (first entry)

DT

XX Human NOVX16e protein.

DE

XX NOVX protein; biochemical stimulation; physiological stimulation;

KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;

KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;

KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;

KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;

KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;

KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;

KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;

KW depression; allergy; fertility disorder; NOVX16e.

XX

OS Homo sapiens.

XX

PN WO2003050245-A2.

XX

PD 19-JUN-2003.

XX

PF 03-DEC-2002; 2002WO-US038594.

XX

PR 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 20-DEC-2001; 2001US-0341540P.

PR 27-DEC-2001; 2001US-0342592P.

PR 31-DEC-2001; 2001US-0344297P.

PR 17-APR-2002; 2001US-0344903P.

PR 15-MAY-2002; 2002US-0373288P.

PR 17-MAY-2002; 2002US-0380981P.

PR 28-MAY-2002; 2002US-0381495P.

PR 28-MAY-2002; 2002US-0383534P.

PR 29-MAY-2002; 2002US-0383744P.

PR 29-MAY-2002; 2002US-0383829P.

PR 07-AUG-2002; 2002US-0384024P.

PR 26-AUG-2002; 2002US-0401788P.

PR 31-OCT-2002; 2002US-0406353P.

PR 02-DEC-2002; 2002US-00406353.

XX

PA (CURA-) CUPAGEN CORP.

XX

PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;

PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;

PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphey R;

PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;

PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;

XX

DR WPI; 2003-513974/48.

DR N-PSDB; ADE95567.

DR

XX New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX

PS Claim 2; SEQ ID NO 100; 211pp; English.

PS

XX This invention relates to novel NOVX proteins, and the DNA sequence which

CC encode them, having properties related to stimulation of biochemical or

XX

CC physiological responses in a cell, a tissue, an organ or an organism.

CC Compounds which modulate the proteins of the invention may have cardiant,

CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,

CC antiarthritic, antidiabetic, nephrotropic, dermatological,

CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,

CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,

CC antidepressant, antiallergic or gynaecological activities. The DNA

CC sequences of the invention may be useful for gene therapy whilst the

CC protein sequences may allow the development of a vaccine. The protein is

CC useful in the manufacture of a medicament for treating a syndrome

CC associated with a human disease. The invention may be useful in

CC diagnosing, treating or preventing NOVX-associated disorders, for example

CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, skin

CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin

CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,

CC Parkinson's disease, asthma, schizophrenia, depression, allergies or

CC fertility disorders. The nucleic acids may further be used as

CC hybridisation probes, in chromosome mapping, tissue typing, preventive

CC medicine, and pharmacogenomics. The present sequence is the amino acid

CC sequence of the human NOVX16e protein of the invention.

XX

XX Sequence 390 AA;

SQ

Query Match 83.4%; Score 337; DB 7; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.4e-297;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPNDVARVLPNGSLFLPAGVIGDEGIFRCQAMNRNGKTSNRYRVVYQIPGKPEIV 127

DB 54 GGGPNDVARVLPNGSLFLPAGVIGDEGIFRCQAMNRNGKTSNRYRVVYQIPGKPEIV 113

QY 128 DSASELTAGVPNKVGTCVSEGSVPAGTLSWHLDDGKPLVNEKGVSKETRHPETGLFT 187

DB 114 DSASELTAGVPNKVGTCVSEGSVPAGTLSWHLDDGKPLVNEKGVSKETRHPETGLFT 173

QY 188 LQSELMVTFARGGDPRTFSCFSFGLPRHRLARTAPIQRYWPEVPLEEVLWVEPEG 247

DB 174 LQSELMVTFARGGDPRTFSCFSFGLPRHRLARTAPIQRYWPEVPLEEVLWVEPEG 233

QY 248 AVAPGGTVTLTCEVPAQSPQIHWKMDGVLPPLPSPVLILPEIPGDDGTTCVATHSS 307

DB 234 AVAPGGTVTLTCEVPAQSPQIHWKMDGVLPPLPSPVLILPEIPGDDGTTCVATHSS 293

QY 308 HGPQESRAVSISIIPEGEGPTAGSVGGGLGTALALGILGLGTAAALLIGVILWQREQ 367

DB 294 HGPQESRAVSISIIPEGEGPTAGSVGGGLGTALALGILGLGTAAALLIGVILWQREQ 353

QY 368 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 404

DB 354 RRGEERKAPENQEEERAEALNQSEPEAGESSTGGP 390

RESULT 15

ADP19670

ID ADP19670 standard; protein; 390 AA.

XX

AC ADP19670;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human LP2007 protein SEQ ID NO:16.

XX

XX human; LP2007; antidiabetic; neuroprotective; nootropic;

KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;

KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;

KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;

KW systemic lupus erythematosus.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..23

Protein /label= signal
24..390
/label= LP2007

W02004044126-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032734.

14-NOV-2002; 2002US-0426253P.

(ELIL) LILLY & CO ELI.

Na S, Perkins DR;

WPI; 2004-411705/38.

N-PSDB; ADP19669.

New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.

Disclosure; SEQ ID NO 16; 111pp; English.

The present sequence represents human LP2007, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 95% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising a therapeutic amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from a disease, condition or disorder associated with aberrant levels of an LP-polypeptide. (C) has anti-rheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive, antidiabetic, neuroprotective, nootropic, antiinflammatory, nephrotropic and dermatologic activities, and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications, autoimmune disease, multiple inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can also be used in manufacturing a medicament for the treatment of the above -mentioned diseases, conditions or disorders associated with aberrant levels of the LP polypeptide.

Sequence 390 AA;

Query Match 83.4%; Score 337; DB 8; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.4e-297;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPWDSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 127
DB 54 GGGPWDSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 113

QY	128	DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHHPETGLFT	187
DB	114	DSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRHHPETGLFT	173
QY	188	LQSELMTVTARGGDPRTPTFSCSFSPGLPRHRLRTAPIQPRVMEPVLEEVQLVVEPEGG	247
DB	174	LQSELMTVTARGGDPRTPTFSCSFSPGLPRHRLRTAPIQPRVMEPVLEEVQLVVEPEGG	233
QY	248	AVAPGGTVTLTCEVPAQPSQPIHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS	307
DB	234	AVAPGGTVTLTCEVPAQPSQPIHMKDGVPLPLPPSPVLILPEIGPQDQGTYSVATHSS	293
QY	308	HGQESRAVSISIIIEPGEGPTAGSVGGSLGTALALGILGGLGTAAALLIGVILMQRRO	367
DB	294	HGQESRAVSISIIIEPGEGPTAGSVGGSLGTALALGILGGLGTAAALLIGVILMQRRO	353
QY	368	RRGEERKAPENQEEERAEELNQSEEPAGESSSTGGP	404
DB	354	RRGEERKAPENQEEERAEELNQSEEPAGESSSTGGP	390

Search completed: December 6, 2004, 15:14:25
Job time : 160 secs

